

## SEQUENCE PROTOCOL

&lt;110&gt; Degussa AG

5 &lt;120&gt; New nucleotide sequences which code for the mikE17 gene

&lt;130&gt; 000561 BT

&lt;140&gt;

10 &lt;141&gt;

&lt;160&gt; 4

&lt;170&gt; PatentIn Ver. 2.1

15

&lt;210&gt; 1

&lt;211&gt; 1890

&lt;212&gt; DNA

&lt;213&gt; Corynebacterium glutamicum

20

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (252)..(1673)

&lt;223&gt; mikE17 gene

25

&lt;400&gt; 1

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gggcggatgt ggcccgacca cgccgggcac ctggtggcgg cgggctgcgt cgaaaagcga 180

aaatcaacaa gtttgcaaca cctcagtgcc aagagtgggt aaggtgatgg tgatcacgct 240

35

atagttgcgc c atg gga aag aca tat gtg ggg tcc agg ctg cgc caa ctg 290

Met Gly Lys Thr Tyr Val Gly Ser Arg Leu Arg Gln Leu  
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cgc cgc gaa aga gac ctg agc cag gca tcc tta gca gca acc ctt ggc 338

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Arg Arg Glu Arg Asp Leu Ser Gln Ala Ser Leu Ala Ala Thr Leu Gly  
15 20 25

tta tct gca agt tat gta aat cag att gag cac gac gta cgc ccg ctc 386

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Leu Ser Ala Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu  
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acc gta ccg gtg tta ttg cgc atc acc gag gcg ttc ggc gta gac gca 434

Thr Val Pro Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala  
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acg ttt ttc tcc cgc gac gat gac tcc cgc ctg ctc gcc gag gtc caa 482

Thr Phe Phe Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln  
65 70 75

55

gac gtc atg ctg gac cgg gag atc aat cct gcg aac gtg gag ctg caa 530

Asp Val Met Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln  
80 85 90

Sub A1

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Sub A1

5	gag ctt tcg gag atg gtg tac aac cac ccc caa cta gcg cgc gcg atg	578
	Glu Leu Ser Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met	
	95 100 105	
10	gtg gaa atg cac cag cgt tac cga aac gtg cgc gat aag ttc tcc atc	626
	Val Glu Met His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile	
	110 115 120 125	
15	gca gtg gat aat cgc acc aac acg cct gag gaa cgc cgt ccc atc gcg	674
	Ala Val Asp Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala	
	130 135 140	
20	gag gcc gtg agc atg ccg cac gaa gag gtc cgc gat ttc att tac gcc	722
	Glu Ala Val Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala	
	145 150 155	
25	cgc caa aac tac ttc gat gcc ctt gac cgc cgc gcc gaa gcc atc gcc	770
	Arg Gln Asn Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala	
	160 165 170	
30	gcg caa ctg ggc tgg cag ccg tac gat tcc cgc gcc atg gaa gat tcg	818
	Ala Gln Leu Gly Trp Gln Pro Tyr Asp Ser Arg Ala Met Glu Asp Ser	
	175 180 185	
35	atc gcc cgc cgc ctg caa atg gat cac gat gtc acc atc acc tcc tcc	866
	Ile Ala Arg Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser	
	190 195 200 205	
40	aaa gag gaa tcc ggc acg ctg cac cac ttc gac ccc gag acg cgt ctg	914
	Lys Glu Glu Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu	
	210 215 220	
45	ctg aca atc cac gca cgc ctc aac ccc ggc caa cgc gcc ttc cgc atg	962
	Leu Thr Ile His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met	
	225 230 235	
50	gcc acc gaa ctc ggc tac cta gaa gcc aac gac ctc atc gaa ggt atc	1010
	Ala Thr Glu Leu Gly Tyr Leu Glu Ala Asn Asp Leu Ile Glu Gly Ile	
	240 245 250	
55	gtt gac gac ggc atc tgg tcc acc ccc gaa gcc cgc acc cta gcc atc	1058
	Val Asp Asp Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile	
	255 260 265	
60	cgc ggt gtg gcc tcc tac ttc gcc gcc gcc gtg atg ctg ccc tac aaa	1106
	Arg Gly Val Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys	
	270 275 280 285	
65	atc ttc cac tcc gag gcc gaa aaa tcc ggc tac gac atc gag tac cta	1154
	Ile Phe His Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu	
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70	ggc caa ctc ttt ggc gtg ggc tat gag aca acc gcc cac cgc ttg tcc	1202
	Gly Gln Leu Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser	
	305 310 315	

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Sub A.1

[illegible]

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10	gtc gac cgc gcc ggc aac atg tcc aaa cgc caa tcc gcc acc ggc ttc	1298
	Val Asp Arg Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe	
	335 340 345	
15	cac ttc acc cac tac ggc ggc acc tgc ccc ctg tgg aac gtg ttt gaa	1346
	His Phe Thr His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu	
	350 355 360 365	
20	acc ttc acc aac ccc ggc caa gtg ctc cgc caa ttc gcg caa atg ccc	1394
	Thr Phe Thr Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro	
	370 375 380	
25	gac gga cgc aac tac ctg tgg atc tca cgc acc gtg cga cac cac gaa	1442
	Asp Gly Arg Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu	
	385 390 395	
30	gcc cgg ttc ggc gaa gta gac aaa atg ttc gcc atc ggc ctg ggc tgc	1490
	Ala Arg Phe Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys	
	400 405 410	
35	gaa gcg cgc cac gcc gac cgc act gtg tac tcc cgc ggt ttc aac ctc	1538
	Glu Ala Arg His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu	
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40	cag gac ctc tcc acc gcc acc ccc atc ggg tcc ggc tgc cga gtg tgc	1586
	Gln Asp Leu Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys	
	430 435 440 445	
45	acc cgc gag aac tgc gcg cag cgc gca ttc cca tcc gtc cac ggc cgc	1634
	Thr Arg Glu Asn Cys Ala Gln Arg Ala Phe Pro Ser Val His Gly Arg	
	450 455 460	
50	atc aac atc gac gcg cac gaa tcc act atc gcg ccg tac taagaaaagg	1683
	Ile Asn Ile Asp Ala His Glu Ser Thr Ile Ala Pro Tyr	
	465 470	
55	agcttgcttt acgacgcacc ctgcgggggt ggggtttacc ttttatgaat gatcagcaat	1743
	atccgcgtaa acaccatcgg tagccagaag aacatcatcc ggggcgataa tcagggacca	1803
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 Ser Tyr Val Asn Gln Ile Glu His Asp Val Arg Pro Leu Thr Val Pro  
 5 35 40 45  
 Val Leu Leu Arg Ile Thr Glu Ala Phe Gly Val Asp Ala Thr Phe Phe  
 50 55 60  
 10 Ser Arg Asp Asp Asp Ser Arg Leu Leu Ala Glu Val Gln Asp Val Met  
 65 70 75 80  
 Leu Asp Arg Glu Ile Asn Pro Ala Asn Val Glu Leu Gln Glu Leu Ser  
 85 90 95  
 15 Glu Met Val Tyr Asn His Pro Gln Leu Ala Arg Ala Met Val Glu Met  
 100 105 110  
 His Gln Arg Tyr Arg Asn Val Arg Asp Lys Phe Ser Ile Ala Val Asp  
 115 120 125  
 Asn Arg Thr Asn Thr Pro Glu Glu Arg Arg Pro Ile Ala Glu Ala Val  
 130 135 140  
 25 Ser Met Pro His Glu Glu Val Arg Asp Phe Ile Tyr Ala Arg Gln Asn  
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 Tyr Phe Asp Ala Leu Asp Arg Arg Ala Glu Ala Ile Ala Ala Gln Leu  
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 180 185 190  
 Arg Leu Gln Met Asp His Asp Val Thr Ile Thr Ser Ser Lys Glu Glu  
 195 200 205  
 35 Ser Gly Thr Leu His His Phe Asp Pro Glu Thr Arg Leu Leu Thr Ile  
 210 215 220  
 40 His Ala Arg Leu Asn Pro Gly Gln Arg Ala Phe Arg Met Ala Thr Glu  
 225 230 235 240  
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 245 250 255  
 45 Gly Ile Trp Ser Thr Pro Glu Ala Arg Thr Leu Ala Ile Arg Gly Val  
 260 265 270  
 Ala Ser Tyr Phe Ala Ala Ala Val Met Leu Pro Tyr Lys Ile Phe His  
 275 280 285  
 50 Ser Glu Ala Glu Lys Ser Gly Tyr Asp Ile Glu Tyr Leu Gly Gln Leu  
 290 295 300  
 55 Phe Gly Val Gly Tyr Glu Thr Thr Ala His Arg Leu Ser Thr Leu Gln  
 305 310 315 320  
 Arg Pro Asn Leu Arg Gly Ile Pro Phe Thr Phe Val Arg Val Asp Arg  
 325 330 335

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Sub A1

Ala Gly Asn Met Ser Lys Arg Gln Ser Ala Thr Gly Phe His Phe Thr  
 340 345 350  
 5 His Tyr Gly Gly Thr Cys Pro Leu Trp Asn Val Phe Glu Thr Phe Thr  
 355 360 365  
 Asn Pro Gly Gln Val Leu Arg Gln Phe Ala Gln Met Pro Asp Gly Arg  
 370 375 380  
 10 Asn Tyr Leu Trp Ile Ser Arg Thr Val Arg His His Glu Ala Arg Phe  
 385 390 395 400  
 Gly Glu Val Asp Lys Met Phe Ala Ile Gly Leu Gly Cys Glu Ala Arg  
 15 405 410 415  
 His Ala Asp Arg Thr Val Tyr Ser Arg Gly Phe Asn Leu Gln Asp Leu  
 420 425 430  
 20 Ser Thr Ala Thr Pro Ile Gly Ser Gly Cys Arg Val Cys Thr Arg Glu  
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